**Evolutionary Genetics Day Trip at Monks Riseborough.**

**Introduction**

In this study we will aim to observe evidence for the action of selection, genetic drift or gene flow on the frequency of shell colour polymorphism in the snail species *Cepaea nemoralis*.

Polymorphism is the occurrence of more than one wild type of allele in a population of a species at a specific gene locus. The four underlying processes which help explain the existence of polymorphism are; genetic drift & selection which account for the spread or loss of allele frequency, mutation which produces different alleles and gene flow which is the movement of alleles from one population to another. Genetic drift itself is a change in allele frequency within a population due to chance, with its effects greater in small populations in comparison to larger ones.

*Cepaea nemoralis* is a land snail that lives in woods and open grasslands hence why the study took place in the Pulpit Hill Reserve, Monks Riseborough, an area consisting of small shrubs sites, as well as open grassland. The species is polymorphic in colour and banding patterns, which range from pink, yellow and brown with the number of bands differing from 0-5.The reason why we are studying snails rather than humans or any other species is due mainly to their slow locomotion over a generation, so many can be found in a small area. Therefore, genetic differences accumulate over short distances allowing us to observe them in one locality. In more mobile moving species such as humans or flies, population genomes are more widely spread hence gene flow is also much greater. Another reason is that the *Cepaea* species, although cross fertilising hermaphrodites (1), have considerable differences in their anatomy (2) and so hybrids between them are very rare (3), making them an ideal model organism when studying species evolution as any genetic differences can be attributed specifically back to each Cepaea species . They are also easier to collect and examine than for example humans, due to their small size in addition to their easily identifiable phenotype (shell banding and colour). In addition, studying humans is rather more complicated due to cost (from analysing data to possible monetary incentives which might be needed to study a large sample of the population), permission and ethical issues which can arise e.g. classifying races and obtaining consent.

We hope to analyse the variations in allele frequency in specific habitats, in the hope to see whether the observations are due to genetic drift, gene selection or gene flow. Comparison will be made to see which of the three underlying processes (genetic drift, selection or gene flow) are affecting the frequency of alleles in specific geographic locations, although it would be difficult to reach to a definite conclusion because of the complexity of the many variables.

We hypothesise that in the open grassland, lighter coloured snails with fewer bands (between 0-3) will be observed, and in habitats consisting of shrubs and short trees we expect to find darker snails with a greater number of bands (4-5). Populations found at the boundaries of habitats will exhibit more composite phenotypic traits due to gene flow. In support of our hypothesis we expect darker colored and 4-5 banded snails in the shrubs, this could be due to selection as such a trait aids camouflage and thus evasion from predators, which gives a selective advantage (4). On the other hand the presence of lighter colored snails with fewer bands may be due to the ability of lighter colored snails to survive better in warmer climates, as they are able to reflect light and appear less conspicuous to predators (2). The differences could also simply be attributed to genetic drift which occurs randomly. If genetic drift is the sole reason for differentiation then the relationship between phenotype and environment should be random and no correlation between the two. Moreover, if it is due to gene flow then there will be multiple polymorphic traits, whereas if selection was acting then there will be limited traits found at specific sites.

Our sampling method will include looking at 3 sites of open grassland and 3 sites of shrubs along the same altitude. Each site was determined by calculating a 3 metre radius and recording observations. Two contingency tables will be drawn up to check for any significant differences which may be contained in the three shrub sites and three open grassland sites. If it can be been established that there are no differences between the sites, a final Chi-squared test can be conducted comparing all the open grassland sites versus all the shrub sites. This will either allow us to accept the initial hypothesis or reject it provisionally at a specific p value.

**References**

1. Aubertin, D. 1927. On the anatomy of the land snails (Helicidae) Cepaea hor- tensis (Mull) and Cepaea nemoralis (L.). Proc. Zool. Soc. London 1927: 553-82
2. Perrot, J.-L., Perrot, M. 1938. Mono- graphie des Helix du groupe Cepaea. Contribution a la notion d'espece. Bull. Biol. Fr. Belg. 72:232-59
3. Lang, A. 1908. Uber die Bastarde von Helix hortensis Mueller und H. nemor- alis L. Festschr. Univ. Jena 1908:1-120
4. Cain, A. J. 1953. Visual selection by tone of Cepaea nemoralis. J. Conchol. 23:333-36
5. Brooker .J.R. (2009). *Genetics Analysis & Principles* 3rd edition. New York: McGraw-hill.